

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/589,870c  
Source: IFC0576  
Date Processed by STIC: 3-29-05

***ENTERED***



IFW16

**RAW SEQUENCE LISTING** DATE: 03/29/2005  
 PATENT APPLICATION: US/09/589,870C TIME: 11:38:08

Input Set : D:\547.app.txt  
 Output Set: N:\CRF4\03292005\I589870C.raw

4 <110> APPLICANT: Goshorn, Stephen C.  
 5       Graves, Scott Stoll  
 6       Schultz, Joanne Elaine  
 7       Lin, Yukang  
 8       Sanderson, James A.  
 9       Reno, John M.  
 11 <120> TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND  
 12      METHODS OF USE THEREOF  
 15 <130> FILE REFERENCE: 110186.547  
 17 <140> CURRENT APPLICATION NUMBER: US 09/589,870C  
 18 <141> CURRENT FILING DATE: 2000-06-05  
 20 <150> PRIOR APPLICATION NUMBER: US 60/168,976  
 21 <151> PRIOR FILING DATE: 1999-12-03  
 23 <150> PRIOR APPLICATION NUMBER: US 60/137,900  
 24 <151> PRIOR FILING DATE: 1999-06-07  
 26 <160> NUMBER OF SEQ ID NOS: 48  
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 31 <211> LENGTH: 638  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: Streptomyces avidinii  
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 37 cgtcggttgc a gccatcgccg tttccctgac cacggctctcg attacggcca gcgcttcggc 120  
 38 agaccccctcc aaggactcga aggccccagg t ctcggccggcc gaggccggca tcaccggcac 180  
 39 ctggtaacaac cagctcggtt c gacccat cgtgaccggcg ggcggccgacg ggcgcctgac 240  
 40 cggAACCTAC gagtcggccg tcggcaacgc c gaggccgc tacgtcctga cggctcgta 300  
 41 cgacacgcgc cccggccacccg acggcaggcg caccggccctc gttggacgg tggctggaa 360  
 42 gaataactac cgcaacgcgc ac tcccgac c acgtggagc ggcaggatcgc tcggccggc 420  
 43 cgaggcgagg atcaacaccc agtggctgct gacccggcc accaccgagg ccaacgcctg 480  
 44 gaagtccacg ctggtcggcc acgacacaccc caccaaggta aagccgtccg cccgcctccat 540  
 45 cgacgcccgg aagaaggccg gctcaacaa cggcaacccg ctcgacgccc ttcagcagta 600  
 46 gtcgcgtccc ggcacccggcg ggtgccggga cctcgcc 638  
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 49 <211> LENGTH: 183  
 50 <212> TYPE: PRT  
 51 <213> ORGANISM: Streptomyces avidinii  
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 56 Ser Ile Thr Ala Ser Ala Ser Ala Asp Pro Ser Lys Asp Ser Lys Ala  
 57               20               25               30  
 58 Gln Val Ser Ala Ala Glu Ala Gly Ile Thr Gly Thr Trp Tyr Asn Gln

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|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 59 | 35  | 40  | 45  |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 60 | Leu | Gly | Ser | Thr | Phe | Ile | Val | Thr | Ala | Gly | Ala | Asp | Gly | Ala | Leu | Thr |
| 61 | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |     |
| 62 | Gly | Thr | Tyr | Glu | Ser | Ala | Val | Gly | Asn | Ala | Glu | Ser | Arg | Tyr | Val | Leu |
| 63 | 65  |     |     |     | 70  |     |     | 75  |     |     |     |     |     |     |     | 80  |
| 64 | Thr | Gly | Arg | Tyr | Asp | Ser | Ala | Pro | Ala | Thr | Asp | Gly | Ser | Gly | Thr | Ala |
| 65 |     | 85  |     |     |     | 90  |     |     |     |     |     |     |     |     |     | 95  |
| 66 | Leu | Gly | Trp | Thr | Val | Ala | Trp | Lys | Asn | Asn | Tyr | Arg | Asn | Ala | His | Ser |
| 67 |     | 100 |     |     |     | 105 |     |     |     |     |     |     |     |     |     | 110 |
| 68 | Ala | Thr | Thr | Trp | Ser | Gly | Gln | Tyr | Val | Gly | Gly | Ala | Glu | Ala | Arg | Ile |
| 69 |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |     | 125 |
| 70 | Asn | Thr | Gln | Trp | Leu | Leu | Thr | Ser | Gly | Thr | Thr | Glu | Ala | Asn | Ala | Trp |
| 71 |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |     | 140 |
| 72 | Lys | Ser | Thr | Leu | Val | Gly | His | Asp | Thr | Phe | Thr | Lys | Val | Lys | Pro | Ser |
| 73 | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     |     | 160 |
| 74 | Ala | Ala | Ser | Ile | Asp | Ala | Ala | Lys | Lys | Ala | Gly | Val | Asn | Asn | Gly | Asn |
| 75 |     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     |     | 175 |
| 76 | Pro | Leu | Asp | Ala | Val | Gln | Gln |     |     |     |     |     |     |     |     |     |
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79 &lt;210&gt; SEQ ID NO: 3

80 &lt;211&gt; LENGTH: 1612

81 &lt;212&gt; TYPE: DNA

82 &lt;213&gt; ORGANISM: Streptomyces avidinii

84 &lt;400&gt; SEQUENCE: 3

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| 85  | gaattcacga  | agtaaccgac   | aggactcgcc | cattcttgg   | ccgaaattcc  | tttgcagaaaa | 60   |
| 86  | atgttgtga   | gaaccctccg   | atggctagta | cgatttacac  | cgaacatgtg  | cccttggcaa  | 120  |
| 87  | ccatcgaccc  | ggacacctcgac | catccagttc | tgccgccaaa  | gacacatgcc  | gcactgctgt  | 180  |
| 88  | ttgttccaccc | acaccgtcag   | gtgcacggcc | gaggtcaca   | accttgcacgg | gcgggatacgg | 240  |
| 89  | gacggcgcac  | gccacagcgc   | gccctccgtc | cccgcgggc   | aacaactagg  | gagtattttt  | 300  |
| 90  | cgtgtctcac  | atgcgcaga    | tcgtcggtgc | agccatcgcc  | gtttccctga  | ccacggcttc  | 360  |
| 91  | gattacggcc  | atggctgaca   | tccagatgac | tcagtcctca  | tcgtccttgc  | ctgcctctgt  | 420  |
| 92  | gggagacaga  | gtcacgatca   | cttgcgggc  | tagtcagggc  | attagaggtt  | atttagactg  | 480  |
| 93  | gtatcagcag  | aaacctggta   | agggaccgaa | actcctaattc | tactccacat  | ccaatttaaa  | 540  |
| 94  | ttctgggtgc  | ccatcaaggt   | tcagtggcag | tgggtctggg  | ttagattata  | ctctcaccat  | 600  |
| 95  | cagcagcctt  | cagcctgaa    | atttcgcaac | gtattactgt  | ctacagcgta  | atgcgtatcc  | 660  |
| 96  | gtacacgttc  | ggacaaggga   | ccaagctgga | gatcaagatc  | tctgggtggc  | gtggctcgcc  | 720  |
| 97  | cgggtgtggg  | tcgggtggc    | gaggctcgag | ccaggttcag  | ctgggtccagt | ctggggcaga  | 780  |
| 98  | ggtaaaaaag  | ccaggggcct   | cagtcaaggt | gtcctgcaag  | gcttctggc   | tcaacattaa  | 840  |
| 99  | agacacctat  | atgcactggg   | tgaggcaggc | acctgacag   | gccctgcagt  | ggatggaaag  | 900  |
| 100 | gattgatcct  | gcgaatggta   | atactaaatc | cgacctgtcc  | ttccaggggca | gggtgactat  | 960  |
| 101 | aacagcagac  | acgtccatca   | acacagccta | catgaaactc  | agcagcctga  | ggtctgacga  | 1020 |
| 102 | cactggcgcc  | tattactgtt   | ctagagaggt | cctaactggg  | acgtggcttt  | tggactactg  | 1080 |
| 103 | gggtcaagga  | accttagtca   | ccgtgagctc | tggctctgg   | tcggcagacc  | cctccaagga  | 1140 |
| 104 | ctcgaaggcc  | caggctctcg   | ccgcccggc  | cggcatcacc  | ggcacctgg   | acaaccagct  | 1200 |
| 105 | cggctcgacc  | ttcatcgta    | ccgcggggc  | cgacggcgcc  | ctgaccggaa  | cctacgagtc  | 1260 |
| 106 | ggccgtcgcc  | aacgcccaga   | gccgctacgt | cctgaccgg   | cgttacgaca  | gcgccccggc  | 1320 |
| 107 | caccgacggc  | agcggcaccg   | ccctcggtt  | gacggtggcc  | tggagaata   | actaccgcaa  | 1380 |
| 108 | cggccactcc  | gcgaccacgt   | ggagcggcca | gtacgtcgcc  | ggcggccgagg | cgaggatcaa  | 1440 |
| 109 | cacccagtgg  | ctgctgaccc   | ccggcaccac | cgaggccaac  | gcctggaagt  | ccacgctgg   | 1500 |

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110 cggccacgac acttcacca aggtgaagcc gtccggcc tccatcgacg cggcgaagaa 1560  
 111 ggccggcgta aacaacggca acccgctcga cgccgttcag cagtaaggat cc 1612  
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 121 Ser Ile Thr Ala Met Ala Asp Ile Gln Met Thr Gln Ser Pro Ser Ser  
 122 20 25 30  
 123 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser  
 124 35 40 45  
 125 Gln Gly Ile Arg Gly Asn Leu Asp Trp Tyr Gln Gln Lys Pro Gly Lys  
 126 50 55 60  
 127 Gly Pro Lys Leu Leu Ile Tyr Ser Thr Ser Asn Leu Asn Ser Gly Val  
 128 65 70 75 80  
 129 Pro Ser Arg Phe Ser Gly Ser Gly Ser Asp Tyr Thr Leu Thr  
 130 85 90 95  
 131 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln  
 132 100 105 110  
 133 Arg Asn Ala Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile  
 134 115 120 125  
 135 Lys Ile Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
 136 130 135 140  
 137 Gly Ser Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 138 145 150 155 160  
 139 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile  
 140 165 170 175  
 141 Lys Asp Thr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
 142 180 185 190  
 143 Gln Trp Met Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Ser Asp  
 144 195 200 205  
 145 Leu Ser Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Ile Asn  
 146 210 215 220  
 147 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val  
 148 225 230 235 240  
 149 Tyr Tyr Cys Ser Arg Glu Val Leu Thr Gly Thr Trp Ser Leu Asp Tyr  
 150 245 250 255  
 151 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Gly Ser Ala  
 152 260 265 270  
 153 Asp Pro Ser Lys Asp Ser Lys Ala Gln Val Ser Ala Ala Glu Ala Gly  
 154 275 280 285  
 155 Ile Thr Gly Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr  
 156 290 295 300  
 157 Ala Gly Ala Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly  
 158 305 310 315 320  
 159 Asn Ala Glu Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro  
 160 325 330 335

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161 Ala Thr Asp Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys  
 162 340 345 350  
 163 Asn Asn Tyr Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr  
 164 355 360 365  
 165 Val Gly Gly Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser  
 166 370 375 380  
 167 Gly Thr Thr Glu Ala Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp  
 168 385 390 395 400  
 169 Thr Phe Thr Lys Val Lys Pro Ser Ala Ala Ser Ile Asp Ala Ala Lys  
 170 405 410 415  
 171 Lys Ala Gly Val Asn Asn Gly Asn Pro Leu Asp Ala Val Gln Gln  
 172 420 425 430  
 174 <210> SEQ ID NO: 5  
 175 <211> LENGTH: 1239  
 176 <212> TYPE: DNA  
 177 <213> ORGANISM: Streptomyces avidinii  
 179 <400> SEQUENCE: 5  
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 181 atgacttgca gggccagtc aagtgttaatg tacatgcact ggtaccagca gaagccagga 120  
 182 tcctccccc aaccctggat ttatgccaca tccaaacctgg cttctggagt ccctgctcgc 180  
 183 ttcagtggtca gtgggtctgg gacctttac tctctcacaa tcagcagagt ggaggctgaa 240  
 184 gatgctgcca ctttattactg ccagcagtttgg attagtaacc caccacgtt cgggtctgg 300  
 185 accaagctgg agctgaagat ctctggtctg gaaggcagcc cggaaaggcagg tctgtctccg 360  
 186 gacgcagggtt ccggctcggag ccaggttcag ctgggtccagt caggggctga gctgggtgaag 420  
 187 cctggggcct cagtgaagat gtcctgcaag gcttctggct acacattttac cagttacaat 480  
 188 atgcactggg taaagcagac acctggacacag ggccttggaaat ggattggagc tattttatcca 540  
 189 gggaaatggtg atacttccta caatcagaag ttcaaaaggca agggccacatt gactgcagac 600  
 190 aaatcctcca gcacagccta catgcagtc agcagcctga catctgagga ctctgcggtc 660  
 191 tattactgtg caagagcgcata attacgaccc aactactggt acttcgtatgt ctggggcgcata 720  
 192 gggaccacgg tcaccgttag ctctggctct ggttcggcag acccctccaa ggactcgaag 780  
 193 gcccagggtct cggccggccga ggccggcattt accggcacct ggtacaacca gtcggctcg 840  
 194 accttcatcg tgaccggcggg cgccgacggc gcccgtaccg gAACCTACGA gtcggccgtc 900  
 195 ggcaacgcgg agagccgcta cgtcctgacc ggtcggtacg acagcgcggcc ggcaccggac 960  
 196 ggcagcggca cggccctcggtt ttggacgggtt ggttggaaataactaccg caacgcggcc 1020  
 197 tcccgacca cgtggagcgg ccagtagtc ggcggccgg aggcggaggat caacaccccg 1080  
 198 tggctgtca cctccggcac caccgaggcc aacgcctgga agtccacgct ggtcggccac 1140  
 199 gacaccttca ccaagggtt ggcgtccggcc gctccatcg acgcggcgaa gaaggccggc 1200  
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 209 1 5 10 15  
 210 Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met  
 211 20 25 30  
 212 His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr  
 213 35 40 45

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214 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
 215 50 55 60  
 216 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu  
 217 65 70 75 80  
 218 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ile Ser Asn Pro Pro Thr  
 219 85 90 95  
 220 Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Ile Ser Gly Leu Glu Gly  
 221 100 105 110  
 222 Ser Pro Glu Ala Gly Leu Ser Pro Asp Ala Gly Ser Gly Ser Ser Gln  
 223 115 120 125  
 224 Val Gln Leu Val Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser  
 225 130 135 140  
 226 Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn  
 227 145 150 155 160  
 228 Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile Gly  
 229 165 170 175  
 230 Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe Lys  
 231 180 185 190  
 232 Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met  
 233 195 200 205  
 234 Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala  
 235 210 215 220  
 236 Arg Ala Gln Leu Arg Pro Asn Tyr Trp Tyr Phe Asp Val Trp Gly Ala  
 237 225 230 235 240  
 238 Gly Thr Thr Val Thr Val Ser Ser Gly Ser Ala Asp Pro Ser  
 239 245 250 255  
 240 Lys Asp Ser Lys Ala Gln Val Ser Ala Ala Glu Ala Gly Ile Thr Gly  
 241 260 265 270  
 242 Thr Trp Tyr Asn Gln Leu Gly Ser Thr Phe Ile Val Thr Ala Gly Ala  
 243 275 280 285  
 244 Asp Gly Ala Leu Thr Gly Thr Tyr Glu Ser Ala Val Gly Asn Ala Glu  
 245 290 295 300  
 246 Ser Arg Tyr Val Leu Thr Gly Arg Tyr Asp Ser Ala Pro Ala Thr Asp  
 247 305 310 315 320  
 248 Gly Ser Gly Thr Ala Leu Gly Trp Thr Val Ala Trp Lys Asn Asn Tyr  
 249 325 330 335  
 250 Arg Asn Ala His Ser Ala Thr Thr Trp Ser Gly Gln Tyr Val Gly Gly  
 251 340 345 350  
 252 Ala Glu Ala Arg Ile Asn Thr Gln Trp Leu Leu Thr Ser Gly Thr Thr  
 253 355 360 365  
 254 Glu Ala Asn Ala Trp Lys Ser Thr Leu Val Gly His Asp Thr Phe Thr  
 255 370 375 380  
 256 Lys Val Lys Pro Ser Ala Ala Ser Ile Asp Ala Ala Lys Lys Ala Gly  
 257 385 390 395 400  
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 261 <210> SEQ ID NO: 7  
 262 <211> LENGTH: 1280  
 263 <212> TYPE: DNA

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